

SEQUENCE LISTING

```
Armstrong, Chris
<110>
       Cohen, Philip
      Methods and Reagents for Assaying Protein Kinase Activity
<120>
      002.0240 (DUNY/P28169PC)
<130>
<140> US 10/510,875
<141> 2005-06-27
<150> PCT/GB03/01286
<151> 2003-03-26
<150> GB 0208104.0
<151> 2002-04-09
      31
<160>
<170>
     PatentIn version 3.1
<210>
       1
<211>
      5
<212>
      PRT
<213> Artificial sequence
<220>
<223> Consensus sequence
<220>
<221>
      MISC FEATURE
<222>
      (4)..(4)
     Any amino acid
<223>
<400> 1
Arg Arg Xaa Ser
<210>
       2
<211>
      6
<212>
      PRT
      Artificial sequence
<213>
<220>
<223>
     Consensus sequence
<220>
<221> MISC_FEATURE
<222> (1)..(1)
```

Page 1

```
<223> R or K
<220>
<221> MISC FEATURE
<222> (2)..(2)
<223> Any amino acid
<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Any amino acid
<220>
<221> MISC FEATURE
<222> (5)..(5)
<223> Any amino acid
<400> 2
Xaa Xaa Arg Xaa Xaa Ser
<210> 3
<211> 6
<212>
     PRT
<213>
     Artificial sequence
<220>
<223>
     Consensus sequence
<220>
<221> MISC FEATURE
<222> (1)..(1)
<223> Any bulky hydrophobic residue
<220>
<221> MISC_FEATURE
<222>
     (2)..(2)
<223> Any amino acid
<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Any amino acid
```

```
MISC FEATURE
<221>
<222> (5)..(5)
<223> Any amino acid
<400> 3
Xaa Xaa Arg Xaa Xaa Ser
<210>
      4
<211>
      10
<212>
      PRT
      Artificial sequence
<213>
<220>
<223>
      Consensus sequence
<400>
      4
Arg Arg Arg Leu Ser Phe Ala Glu Pro Gly
      5
<210>
<211>
      5
<212>
      PRT
<213>
      Artificial sequence
<220>
<223>
      Consensus sequence
<220>
<221> MISC_FEATURE
<222>
      (1)..(1)
<223> Any amino acid
<220>
<221> MISC FEATURE
<222>
      (2)..(2)
<223> Phosphorylated serine
<220>
<221>
      MISC_FEATURE
<222>
       (3)..(3)
<223>
      Any amino acid
<220>
```

<220>

```
<221> MISC_FEATURE
<222> (4)..(4)
<223> Any amino acid
<400> 5
Xaa Xaa Xaa Ser
<210> 6
<211> 7
<212> PRT
<213> Artificial sequence
<220>
<223> Consensus sequence
<400> 6
Leu Ser Phe Ala Glu Pro Gly
<210> 7
<211> 7
<212>
     PRT
<213> Artificial sequence
<220>
<223> Consensus sequence
<220>
<221> MISC FEATURE
<222> (2)..(2)
<223> Phosphorylated serine
<400> 7
Leu Xaa Phe Ala Glu Pro Gly
<210> 8
<211> 5
<212> PRT
<213>
     Artificial sequence
<220>
<223> Consensus sequence
```

```
<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Arg or Lys
<220>
<221> MISC_FEATURE
\langle 222 \rangle (2)...(2)
<223> Arg or Lys
<220>
<221> MISC_FEATURE <222> (3)..(3)
<223> Arg or Lys
<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Any amino acid
<400> 8
Xaa Xaa Xaa Ser
<210> 9
<211> 6
<212> PRT
<213> Artificial sequence
<220>
<223> Consensus sequence
<220>
<221> MISC FEATURE
<222> (1)..(1)
<223> Arg or Lys
<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Arg or Lys
<220>
<221> MISC_FEATURE
<222> (2)..(2)
```

```
<223> Any amino acid
<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Any amino acid
<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Any amino acid
<400>
Xaa Xaa Xaa Xaa Ser
<210>
     10
<211>
      11
<212>
      PRT
<213>
     Artificial sequence
<220>
<223> Consensus sequence
<220>
<221> MISC FEATURE
<222>
      (2)..(2)
<223> Any amino acid
<220>
<221> MISC_FEATURE
<222>
      (4)..(4)
<223> Any amino acid
<400>
      10
Tyr Xaa Thr Xaa Leu Ser Phe Ala Glu Pro Gly
                5
                                    10
<210>
      11
<211>
       11
<212>
      PRT
<213>
      Artificial sequence
<220>
```

```
<223> Consensus sequence
<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Any bulky hydrophobic residue
<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> any amino acid
<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> any amino acid
<400>
      11
Xaa Xaa Tyr Xaa Leu Ser Phe Ala Glu Pro Gly
<210>
      12
<211> 10
<212> PRT
<213>
     Artificial sequence
<220>
<223> Consensus sequence
<220>
<221> MISC FEATURE
<222> (1)..(1)
<223> Any amino acid
<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Any amino acid
<220>
<221>
      MISC_FEATURE
<222>
      (2)..(2)
<223>
      Phosphorylated serine
<400>
      12
```

```
Xaa Xaa Xaa Leu Ser Phe Ala Glu Pro Gly
<210>
      13
<211>
      13
<212>
      PRT
<213>
      Artificial sequence
<220>
<223>
       Consensus sequence
<400>
      13
Lys Lys Leu Asn Arg Thr Leu Ser Phe Ala Glu Pro Gly
<210>
       14
<211>
      7
<212>
      PRT
<213>
       Artificial sequence
<220>
<223>
      Consensus sequence
<220>
       MISC_FEATURE
<221>
<222>
      (2)..(2)
<223>
       phosphoserine
<400>
       14
Leu Xaa Phe Ala Glu Pro Gly
<210>
      15
<211>
<212>
       PRT
<213>
       Artificial sequence
<220>
<223>
      Consensus sequence
<220>
       MISC_FEATURE
<221>
<222>
       (2)..(2)
<223>
       Phosphoserine
```

```
<400> 15
Leu Xaa Ser Pro Ala Glu Pro Gly Cys
                 5
<210>
       16
<211>
       11
<212>
      PRT
<213>
      Artificial sequence
<220>
<223>
      Consensus sequence
<400>
       16
Arg Ala Arg Thr Leu Ser Phe Ala Glu Pro Gly
                5
<210>
      17
<211>
<212>
       PRT
<213>
      Artificial sequence
<220>
<223>
      Consensus sequence
<220>
       MISC_FEATURE
<221>
<222>
       (2)..(2)
<223>
       Phosphoserine
<400>
       17
Leu Xaa Phe Ala Glu Pro Gly Cys
<210>
      18
<211>
       11
<212>
       PRT
<213>
       Artificial sequence
<220>
<223>
      Consensus sequence
<400>
       18
Gly Arg Pro Arg Thr Ser Ser Phe Ala Glu Gly
                                     10
```

```
<210>
       19
<211>
      7
<212>
      PRT
<213>
       Artificial sequence
<220>
<223>
       Consensus sequence
<400>
       19
Leu Arg Arg Ala Ser Leu Gly
<210>
       20
<211>
       32
<212>
       PRT
<213>
      Artificial sequence
<220>
<223>
       Consensus sequence
<400>
       20
Lys Glu Ala Lys Glu Lys Arg Gln Glu Gln Ile Ala Lys Arg Arg Arg
Leu Ser Ser Leu Arg Ala Ser Thr Ser Lys Ser Gly Gly Ser Gln Lys
            20
                                 25
                                                       30
<210>
      21
<211>
       10
<212>
       PRT
<213>
       Artificial sequence
<220>
<223>
       Consensus sequence
<400>
       21
Lys Lys Leu Asn Arg Thr Leu Ser Val Ala
                 5
                                      10
<210>
       22
<211>
       10
<212>
       PRT
<213>
       Artificial sequence
<220>
```

```
<223> Consensus sequence
<400>
       22
Lys Lys Leu Arg Arg Thr Leu Ser Val Ala
                 5
<210>
       23
<211>
       23
<212>
      PRT
<213>
      Artificial sequence
<220>
<223>
       Consensus sequence
<400>
       23
Lys Lys Lys Val Ser Arg Ser Gly Leu Tyr Arg Ser Pro Ser Met Pro
                                      10
Glu Asn Leu Asn Arg Pro Arg
<210>
      24
<211>
       15
<212>
      PRT
<213>
       Artificial sequence
<220>
<223>
       Consensus sequence
<400>
       24
His Met Arg Ser Ala Met Ser Gly Leu His Leu Val Lys Arg Arg
                                                           15
                                     10
<210>
      25
<211>
       11
<212>
       PRT
<213>
       Artificial sequence
<220>
<223>
       Consensus sequence
<400>
       25
Met His Arg Gln Glu Thr Val Asp Cys Leu Lys
                                     10
```

```
<210>
       26
<211>
       11
<212>
       PRT
<213>
       Artificial sequence
<220>
<223>
      Consensus sequence
<220>
      MISC_FEATURE
<221>
<222>
      (6)..(6)
<223> Phosphoserine
<400>
       26
Arg Ala Arg Thr Leu Xaa Phe Ala Glu Pro Gly
<210>
      27
<211>
       10
<212>
      PRT
<213>
      Artificial sequence
<220>
<223>
       Consensus sequence
<220>
<221>
       MISC_FEATURE
<222>
       (5)..(5)
<223>
       Phosphoserine
<400>
       27
Arg Arg Arg Leu Xaa Phe Ala Glu Pro Gly
                                     10
<210>
       28
<211>
       4
<212>
      PRT
<213>
      Artificial sequence
<220>
<223>
       Consensus sequence
<220>
<221>
       MISC FEATURE
       (3)..(3)
<222>
<223>
       Thr or Asn
```

```
<400> 28
Pro Pro Xaa Lys
<210>
       29
<211>
       11
<212>
      PRT
<213>
      Artificial sequence
<220>
<223> Consensus sequence
<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> any amino acid
<220>
<221> MISC_FEATURE
\langle 222 \rangle (4)...(4)
<223> any amino acid
<400>
      29
Arg Xaa Arg Xaa Leu Ser Phe Ala Glu Pro Gly
<210>
      30
<211>
       11
<212>
      PRT
      Artificial sequence
<213>
<220>
<223>
      Consensus sequence
<220>
<221> MISC FEATURE
<222>
      (1)..(1)
<223>
      Any bulky hydrophobic residue
<220>
<221> MISC FEATURE
<222>
      (2)..(2)
<223> any amino acid
```

```
<220>
<221>
      MISC FEATURE
<222>
      (4)..(4)
<223>
       any amino acid
<400>
       30
Xaa Xaa Arg Xaa Leu Ser Phe Ala Glu Pro Gly
                5
<210>
      31
<211>
      13
<212>
      PRT
<213>
      Artificial sequence
<220>
<223> Consensus sequence
<220>
      MISC_FEATURE
<221>
<222>
      (8)..(8)
<223>
      Phosphoserine
<400>
      31
Lys Lys Leu Asn Arg Thr Leu Xaa Phe Ala Glu Pro Gly
                                    10
```